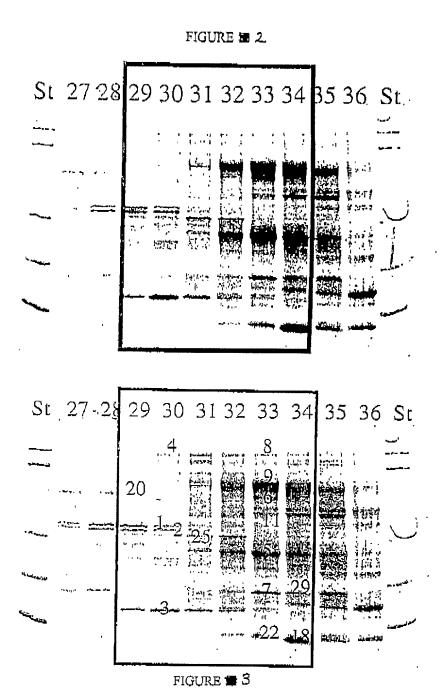
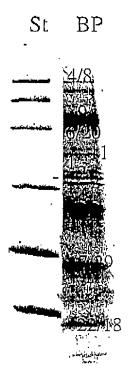
E.





Band No.	Identity
1	histone H1.c
2	lustone H1.c
3	ribosomal protein RS20
4	similar to ribosomal protein LORP
5	BMP-3
6	o2 macroglobulin RAP & BMP-3
7	similar to ribosomal protein LORP
8	BMP-3
9	ВМР-3
11	ribosomal protein RL6 & BMP-3
18	TGF-β2/SPP24
20	Factor H
22	TGF-β2
25	BMP-3 & H1.x
29	BMP-3 & ribosomal protein RL32

FIGURE \$4

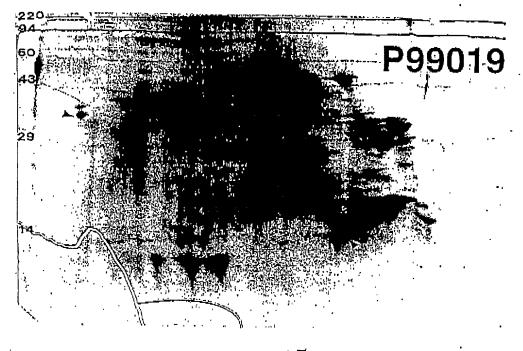
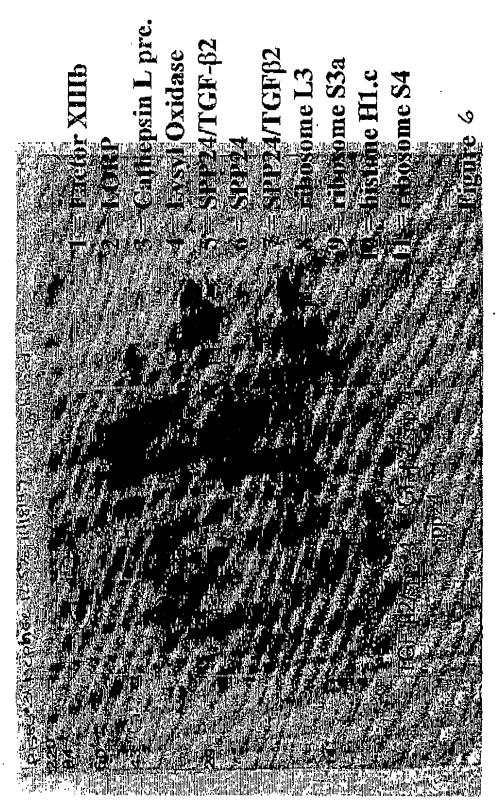
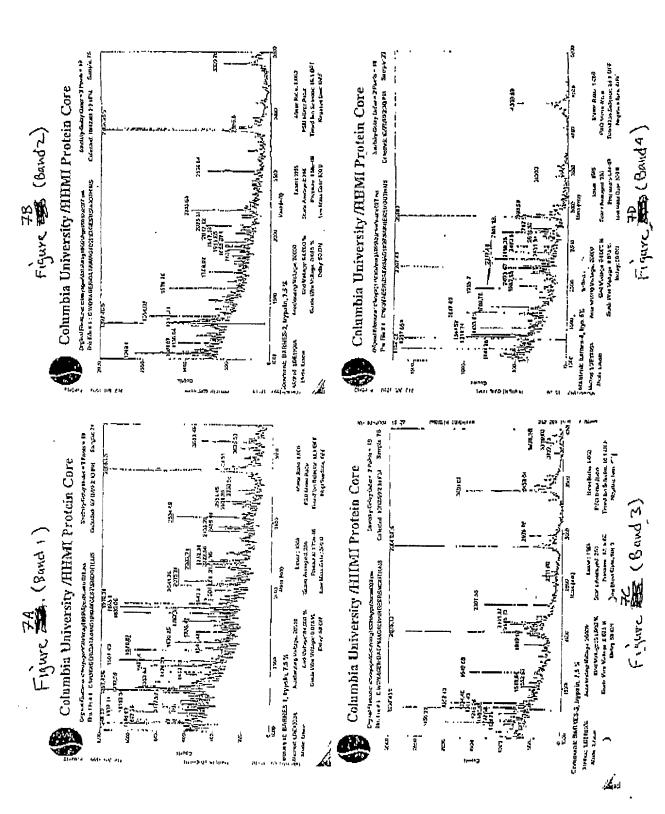
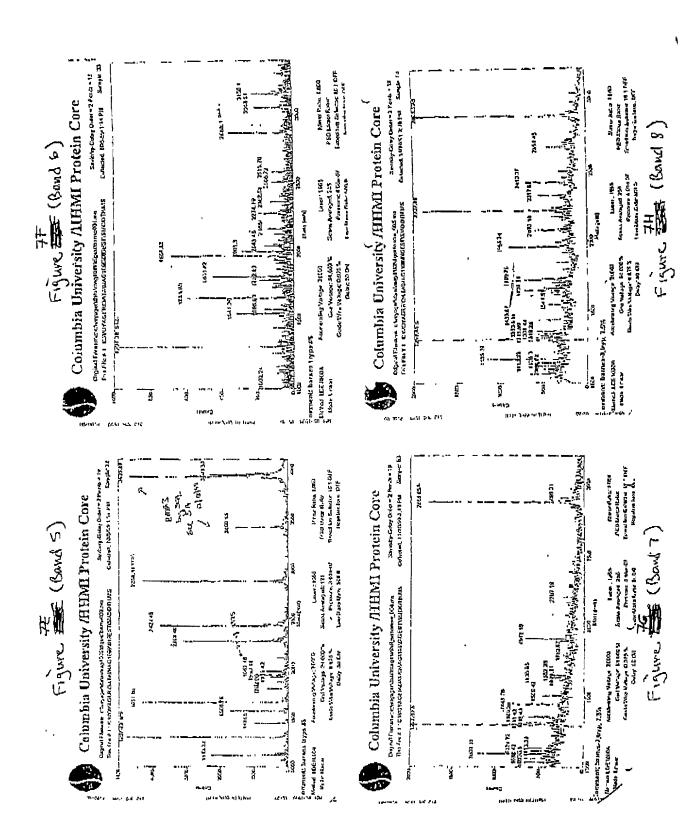


figure 🕿 5

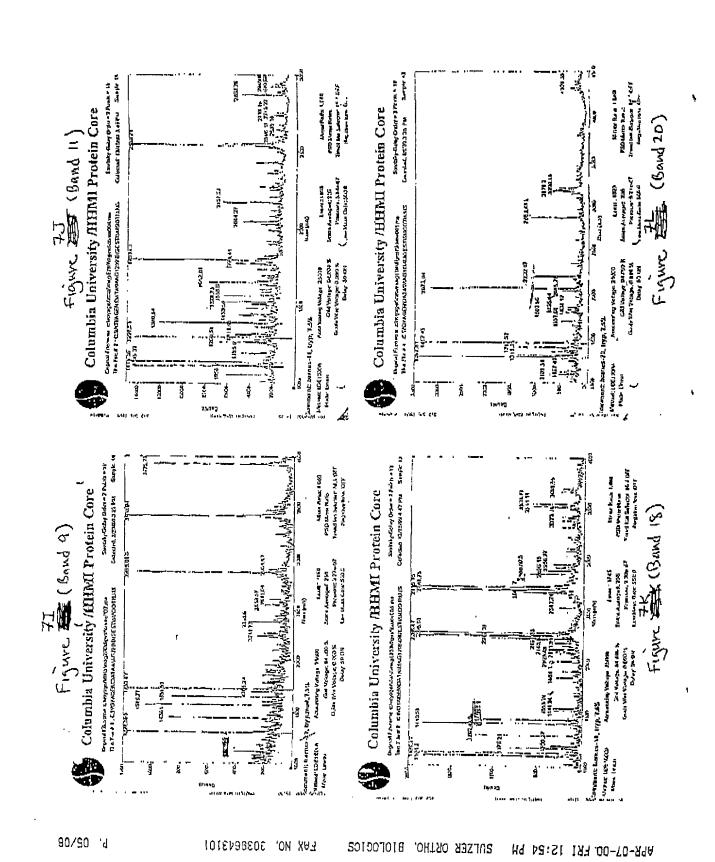


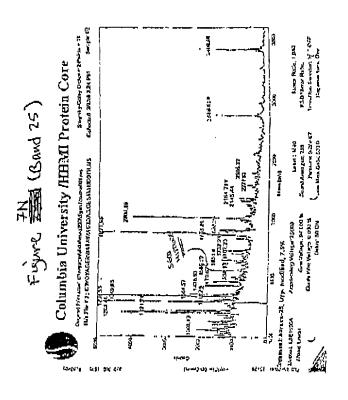
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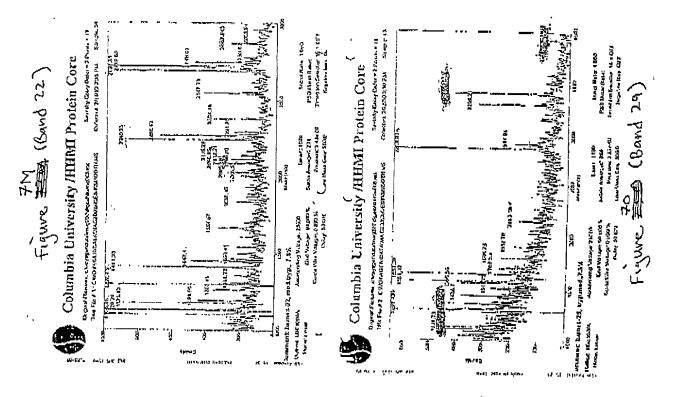


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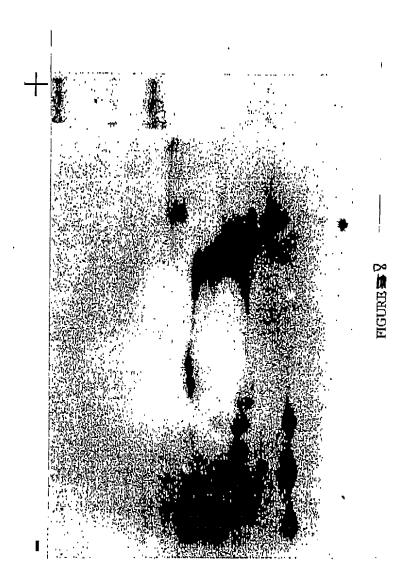


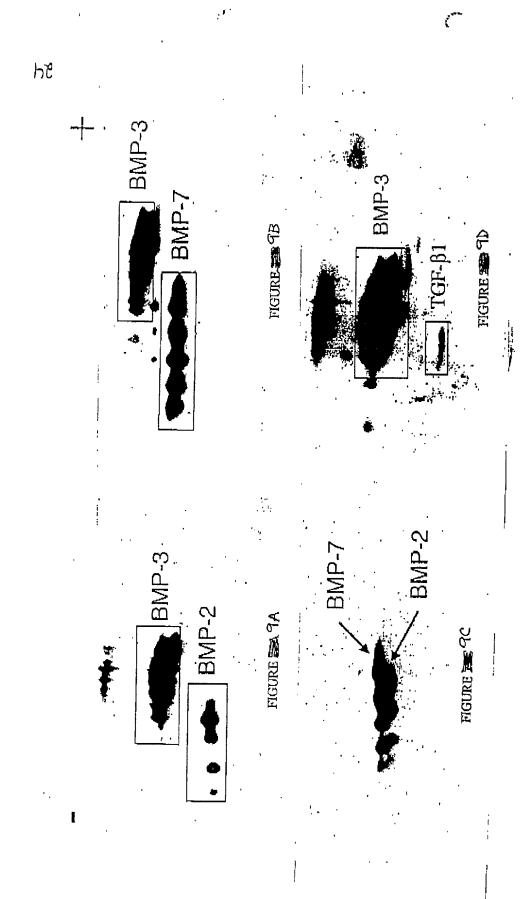


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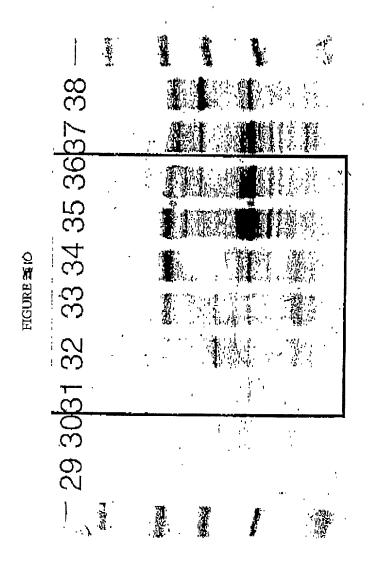


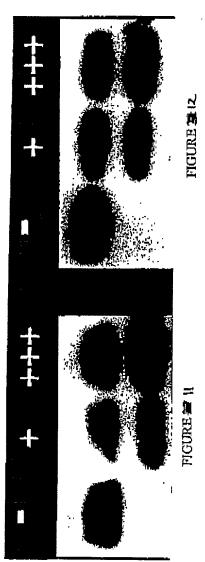
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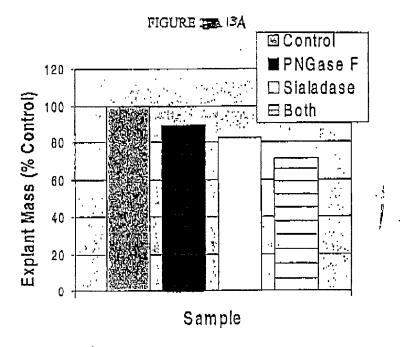


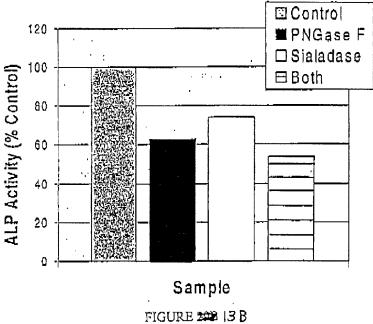


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Figure |4 Antibody Listing

TGF-b1 (burnan) F	0			ממחור בי	Catalog Ivn.
		Species		•)
	Protein	Rabbit	Polyclonal	Promega	G1221
	Peptide	Rabbit		Santa Cruz Biotechnology	06-35
TGE-b3 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-82
	_				
BMP-2 (haman)	Protein	Rabbit	Polyclonal	Austral Biologics	PA-513-9
	Peptide	Chicken	Polyclonal	Research Genetics	NA
	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-6896
HMP-5 (human) P	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sp-7405
	Peptide	Mouse	Monoclonal	Novocastra Laboratories	NCL-BMP6
ВМР-7 (пляза)	Peptide	Rabbit	Polycional	Research Genetics	NA
FGF-1 (human)	Peptide	Goat	Pulyclonal	Sarta Cruz Biotechnology	sc-1884
osteonectin (bovine) (P	Protein	Mouse	Monoclonal	DSHB	AON-1
osleocalcin (bovine) P	Protein	Rabbit	Potycional	Accurate Chemicals	A761R1H
ine)	Protein	Rabbit	Polyclonal	Chemicon International	AB870
transferin (human)	Protein	Chicken	Polyclonal	Chemicon International	AB797
lipoprotein	Protein	Goat	Polyclonal	Chemicon International	AB740
(mman)					~~~

Figure 15A Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Band Sample	Sequence Data	Best Database Match Match Identification	Match	Identification	Species	Acc. No.	AAs
÷								
7	fx 49 (1579)	XI AAAGYDVEK	ALAAAGYDVEK	11/11	histone H1.c	់ កាមការបាំ	87568 (NCBI)	65-75
м	ά 67 (1346)	SLEKYCADLIR	SLEKVCADLIR	11/11	40s Ribosomat Profein S20	ध्य	R3RTZD (PIR)	31-41
7	0 59 xJ	(V)VCGMLGFPSEAPV VVCGMLGFPGEKRV 11/14	VVCGMLGFPGEKRV	17/14	LORP	esnow	AAC95338 NCB()	213
<u>بن</u>	N terminal seq	STGVLLPLONNELPG	STGVILP LONNEL PG 15/15	15/75	ВМР-3	human	4557371 (NCBI)	33.50
	6x 72 (3925)	STGVLLPLONNELPGA EYQY	STGVELPLONNELPG 20/20 AEYQY		BMP-3	homean	4557371 (NCBI)	8 8
	fx 74 (3409)	STGVLLPLQ	STGVILPLO	6/6	вир-з	human	4557371 (NCBI)	290- 298
9	6c 55 (1586)	(s)атсағке	SQTLQFDE	7/6	ВМР-3	human	4557371 (NCBI)	346- 353
	fx 47	WYAF	no match		m			
	N terminal seq	HAGKYSREKNT(P)A(P))	HGGKYSREKNOPKP 11/14		a2-Macroglobulin Receptor Assoc. Pro.	វាមានា	P30533 (Swiss-Prot)	31-46
	lk 57 (1438)	saт <u>t</u> ағреа	son of dea	6/6	вир-з	buman	4557371 (NCBI)	346- 354
	(ZSB) 12 21	SLKPSNHA	SLKPSNMA	878	BMP-3	ритал	4557371 (NCBI)	\$ £
P	tx 51 (1093)	AALRPLVKP	AAŁRPLVKP	£/6	60s Ribosomal Protein L32	тоиѕе	P17932 (Sviss-Prot)	6
	6x 37 (no NS)	A(H)I(Q)VERYV	AIVER	5/5	60s Ribosomni Protein 132	asnow	P17932 (Swiss-Prol)	13 13
	fx 37 (no MS)	A(H)I(Q)VERYV	НОЅВКУV	27	60s Ribosomal Protein L32	eshou	P17932 (Swiss-Prof)	22-28
8	lx 78 0	XALGPI	no match		777			
	fx 58 (1587)	Satlafdeat	Satlafdeat	10/10	BMP-3	human	P12645 (Swiss-Prot)	346- 355

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Figure 15 B Identification of Profesion by Amino Acid Sequencing of Tryptic Fragments from ID Gels

SQTLXF SQTLQF 5/6 BMP-3 human VLATVTKPVGGDK VLATVTKPVGGDK 13/13 80s Ribosomal Protein LG human xVFAL VFAL 4/4 60s Ribosomal Protein LG human AVPQLQGYLR 4/4 60s Ribosomal Protein LG human AVPQLQGYLR 4/4 60s Ribosomal Protein LG human AUDAAYCFR 4/10 50s Ribosomal Protein LG human AUDAAYCFR 4/10 50s Ribosomal Protein LG human GYNANFCAGACPYL 6YNANFCAGACPYL 14/14 TGF-B2 human MNSQSLSPY 9/9 TGF-B2 human MNSQSLSPY 9/9 SPP24 bovine MAARPSV(P) KAARPSV(P) KAARPSV(P) human	Rand	Band Sample	Sequence Data	Best Database Match Match Identification	Watch		Species	ACC, No.	AAS
(1311) Kx 47 VIATVTKPVGGDK VLATVTKPVGGDK VLATVTKPVGGDK VFAL 4/4 60s Ribosomal Protein LG IMMan (1785) Kx 56 ALDAAYCFR 6x 58 ALDAAYCFR 6x NASQSLSFY 6x 68 ALDAAYCFR 6x 68 ALDAA	E	fx 55				BMP-3	human	4557371	346- 354
Kx 47 VIATVTKPVGGDK VLATVTKPVGGDK 13/13 803 Ribosomal Profein LG hunnan 17/12; Kx 76		(1311)						إالاحتمار	3
(1712) xVFAL VFAL 4/4 60s Ribosomal Protein L6 human (1785) KAARPOLQGYLR 4/4 60s Ribosomal Protein L6 human (1145) KABROLQGYLR 44POLQGYLR 9/10 60s Ribosomal Protein L6 human (1145) KAS ALDAAYCFR ALDAAYCFR ALDAAYCFR Human (1101) KAS ALDAAYCFR ALDAAYCFR Human human (1101) KAS BID TGF-B2 human (1101) KAS BIP TGF-B2 human (1101) KAAKPSVP BIP Histone Hf.x human (1411.71) KAAKPSVP BIB Histone Hf.x human (1470) BIB Histone Hf.x human		12.47				80s Ribosomal Protein LG	human	C02878	67-93
fx 76 xVFAL VFAL 4/4 60s Ribosomal Protein L6 human (1785) AVPQLQGYLR 44POLQGYLR 9/10 50s Ribosomal Protein L6 human (1145) ADAAYCFR ALDAAYCFR 5/9 TGF-β2 human (1101) K 58 ALDAAYCFR ALDAAYCFR 5/9 TGF-β2 human (1101) K 58 NNSQSLSPY 9/9 TGF-β2 human (1101) K 58 NNSQSLSPY 9/9 SPP24 human (1411-71) K 58 KAAKPSV(P) KAAKPSVP 9/9 FISTONE H/I.X human (14170) K 39 KAAKPSVP B/B FISTONE H/I.X human		17772						(Swiss-Prot)	
(1785) AVPQLQGYLR 4tPOLQGYLR 9/10 508 Ribosomal Prctain LB human (1145) K58 ALDAAYCFR ALDAAYCFR 9/9 TGF-B2 human (1101) K58 ALDAAYCFR ALDAAYCFR 9/9 TGF-B2 human (1101) K58 (no GYNANFCAGACPYL GYNANFCAGACPYL GYNANFCAGACPYL Human K58 NNSQSLSPY 9/9 SPP24 human K68 NNSQSLSPY 9/9 SPP24 bovine (1411.71) KAAKPSV(P) KAAKPSVP B/B Histone Hfix human (1470) KAARPSV(P) KAAKPSVP B/B Histone Hfix human		14 A				60s Ribosomal Protein L6	human	002878	273
tx 51 AVPQLQGYLR AIPOLQGYLR 9/10 50s Ribosomal Protein L6 human (1145) K 58 ALDAAYCFR ALDAAYCFR 9/9 TGF-B2 human (1101) K 58 ALDAAYCFR ALDAAYCFR 9/9 TGF-B2 human (1101) K 58 NNSQSLSPYL GYNANFCAGACPYL 14/14 TGF-B2 human IX 58 NNSQSLSPY 9/9 SPP24 bovine (1411.71) KAAKPSV(P) KAAKPSVP 9/9 Histone Hf.x human (1470) R 58 Histone Hf.x human		(1785)						(Swiss-Prof)	9/2
(1145) ALDAAYCFR ALDAAYCFR IGF-B2 humbn (1101) K 58 ALDAAYCFR 9/9 TGF-B2 humbn (1101) K 58 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-B2 humbn IX 58 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-B2 humbn IX 58 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-B2 humbn IX 56 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-B2 humbn IX 59 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-B2 humbn IX 50 (14.11.71) KAARPSV(P) KAARPSVP B/B Histone Hff.x humbn (14.70) Humbn Humbn Humbn humbn humbn		tx 51	AVPOLOGYLR			80s Ribosomal Protain L6	human	0.02878	262
6x 58 ALDAAYCFR ALDAAYCFR 9/9 TGF-B2 human (1101) K 59 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 59 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 56 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 56 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 59 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 59 (no GYNANFCAGACPYL GYNANFCAGACPYL I4/14 TGF-B2 human IX 50 (no GYNANFCAGACPYL I4/14 TGF-B2 Human human IX 50 (no GYNANFCAGACPYL <td></td> <td>(1145)</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>(Swiss-Prof)</td> <td>27.7</td>		(1145)						(Swiss-Prof)	27.7
6x 58 ALDAAYCFR ALDAAYCFR 4LDAAYCFR 4/10 mmm 4/10 mmm 4/11 mmm 4/11 mmm 4/14 mmm	1.8								
(1101)	2	£ 5	ALDARYCFR		9/9	TGF-B2	human	P08112	303-
K 59 (no GYNANFCAGACPYL GYNANFCAGACPYL 14/14 TGF-II2 human metch) K 56 WNSQSLSPY 9/9 SPP24 bovine (1411.71) KAAKPSV(P) KAAKPSVP 8/9 Fistore Hf.x human (1470) (1470) AAAKPSVP AAAKPSVP AAAKPSVP AAAKPSVP AAAKPSVP AAAKPSVP AAAKPSVP AAAAKPSVP AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	<u> </u>	(1) (1) (1) (1) (1) (1) (1) (1)				•		(Swiss-Prot)	311
match MNSQSLSPY 9/9 SPP24 bovine (1411.71) KAAKPSVP 6/19 Fistone Hf.x human (1470) human hum		Fr 50 fnn	GYNANFCAGACPYI	GYNANFCAGACPYL	14/14	TGF-II2	human	P08112	340-
fx 65 WNSQSLSPY VNSQSLSPY 9/9 SPP24 bovine (1411.71) KAAKPSV(P) KAAKPSVP 8/8 Histone Hf.x human (1470) (1470) 		match)						(Swiss-Prof)	<u>88</u>
(1411.71) (K 39 KAAKPSV(P) KAAKPSVP BIB (-listone 141.x human (1470)		£ 55	WASTSTSPY		6/6	SPP24	bovine	027967	42-50
(k 39 (KAAKPSV(P) KAAKPSVP 8/B Histone H1.x human (1470)		(1411.71)						(Swiss-Prof)	
29	25	(K 39	KAAKPSV(P)	KAAKPSVP	8/B	Histone Hf.x	human	JC4926 (PIR)	g 28
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Figur 1/4 Identification of Proteins by Mass Spectrometry of Trypfic Fragments from 1D Gels

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Comments	!		15 MS peaks match with Band 2					identification of starred	peplide confirmed by sequence analysis	•	15 MS peaks match with Band 1									12 MS peaks-metch with	Band 8	- 4	-	
% Cover-	206	,	Ø					16				62								8		1		•
AAS			110-121		62-79	64-79	35-54	65-79		64-79	35-54	50-59		76-83	93-93 93-93	8B-89	9-21	5-21	88-119	150-167			648-669	455-478
Mass Diff.	erence		D.60		0,16	0.58	-0.74	0,05		0.13	-0.20	0,36		-0.09	-0.16	0.55	720	-0.17	-0.85	-0.32			-0.28	0.47
Wass	Spec	Database	1172.37		1579.71	1707,89	2012.32	1579.71	· · · · · ·	1707.89	2012.32	1129.40		1156.30	1334,62	1351,58	1517.77	1919,19	3404.87	1988.27			2410.63	2610.10
Mass	Spec	Data	1172.97		1579.87	1708.47	2011.58	1579.76		1708.02	2012.12	1129.76		1158.21	1334,46	1352,13	1518.04	1819,02	3404.02	1997.95			2410.35	2610.57
Acc. No.			87668 (ACBI)	•				87668	(NCBI)			R3RTZ0 (P.IR)								NP002309	Smiss	<u> </u>		
Species Acc. No.			ramud					វាបាកឧព				國								Duman				
Mass Spet	Profile		4 peaks match with	histone H1.c			,	3 peaks	maich with histone H1.c	-		7 peaks match with	nbosome S20							3 peaks		Cysyl Oxidase RP		
Band			-					7				e								Ā				

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Figure, 16B Identification of Proteins by Mass Spectrometry of Tryptic Frugments from ID Gets

Comments	,	% coverage calcufation is relative to the mature BMP-3, 183 AAS (290-472)						identification of starred	peplide confirmed by sequence analysis								% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)		
% Cover-	age	48									Įļ.						5		
AAS		361-368	346-357	345-557	410-424	346-350	374-392	373-392		290-318-	283-290				129-150	257-282	346-357	410-424	
Mass Diff-	ецевсе	0.01	-0.05	0,00	-0.05	70.0	-0.17	-0.36		1.38	0.09				0.15	-0.01	0,18	-0.03	
Mass	Spec	1113.31	1438,58	1566.76	1651.91	1794.02	2268.63	2424.81	<u> </u>	3407.77	1002.15	, ,			236243	3048.52	1566.75	1651.91	
Mass	Spec	1113,32	1438.53	1566.76	1651.85	1794.09	2258.45	2424.45		3409.15	1002.24				2362.58	3048,51	1566.93	1651,88	
Acc. No.		4557374 (NCBI)								-	P30533	(Swiss-	Prot)				4557371 (NCBI)		
Species		human									human						human		
Mass Spec	Profile	9 peaks match with BMP-3									3 peaks	match with	Ę,	Macroglobali n RAP			2 peaks match with BMP-3		
Band		ភេ									9								

Figure 16C Identification of Proteins by Mass Spectrometry of Terptic Fragments from 1D Gels

Cornments								% coverage calculation is relative to the mature BMP-3, 183 AAS (290.472)					12 MS peaks match with Barai 4	% coverage calculation is relative to the mature BMP-3, 183 AAS (280-472)					
% Cover-	age		E					24					e	, 9E				<i>Ì</i>	
AAs			67-75		1-10	65-74	19-28	102-111	361-368	190-200	410-424	346-360	645-669	896-196	346-357	345-357	410-424	41-66	290-318
Mass Diff-	erence		0.08		60'6-	0.44	0.12	0,22	80.0	-0.32	1250	-0.40	9Z (P	51.0-	0.02	0.01	0.30	0.48	1.17
Mass	Sper	Database	1033.17	. B. 64. AMB	1093.40	1134.28	1449.68	1060.20	1113.31	1360.58	1651.93	1794.02	2410.63	1113.31	1438.58	1566.76	1651.61	2901.19	3407.77
Mass	Spec	-	1033.25		1093.31	1134 72	1449.78	1050.42	1113.39	1360.26	1652.28	1793.62	2410.37	1113.14	1438.60	1586.77	1651.91	7901.67	3408.94
Acc. No.			P17932	Prof)				4557371 (NCBI)					NPG02309 (Swiss- Prol)	4557371 (NCBI)					
Species	•		asnow					human					human	firmen .				·····	
Mass Spec	Profile		4 peaks	match with ribosome L32				5 peaks match with BMP-3					1 peak matches with Lysyl Oxidase RP	6 peaks match with BMP-3					
Band			1										60	o.					

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Figure 16D Identification of Proteins by Mass Spectrometry of Tryptic Fragments from 1D Gels

					•																					
Comments			% coverage calculation is	refetive to the mature BMP- 3, 183 AAS (290-472)																			-4-1			
% Cover-	306	'	48						16							25					S		1			
AAs			361-358		410-424	346-360	373-392	290-318	114-122		141-155	10-20		262-271	260-271	303-311		400-409	312-328	340-382	42-53		113-124	BG-58		
Mass Diff-	erence		-0.D8		-0.18	-0.44	-0.57	0.57	0.15		D-02	0.03		D.01	90'0	9070-		-0.16	-0.23	-0.21	-0.6T		-0.0e	10.0	50.05	-0.10
Mass	Spec	Database	1113,31		1651.91	1794.02	2424.81	3407.77	1140.23		1526.88	1059.12		1145.35	1386.68	1101.26		1175.42	2240.80	2691.91	1411,60		1447.65	1540.60	1869.05	2268.57
Mass	Spec	Data	1113,23		1651.73	1793.58	242424	3408.34	1140.38		1526.88	1059.15		1145.38	1386.74	1101.20		1175.26	2240.37	2691.70	1410.93		1447.59	1540.94	1869.10	2268.47
Acc. No.		 	4557371	(NCBI)					Q0287B	(Swiss- Prot)	•	P47911	(Swiss-	•		P08172	(Swiss- Prof)				027967	(Swiss-	<u>.</u>			
Species			ришаи						भागमध्य			ROUSe				human					bovine					
Mass Spec			5 peaks	match with BMP-3					5 peaks	match with ribosome L6			٠			4 peaks	match with TGF-82				5 peaks	match with				
Band			11													18										

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Figure. 16E Identification of Proteins by Mass Spectrometry of Tryptic Fragments from ID Gels

Comments																	% coverage calculation is	12) 183 AAS (290-472)				
% Cover-	ಷ್ಟರ	23	2						11			14					34		•			
AAS		903 244	?		400-409	312-347	312-328	340-362	42-53		113-124	48-57	107-118	107-119	48-58	43-57	102-111		346-357	345-357	410-424	290-318
Mass Diff.	erence	1070	7		-0.29	-0.28	-0.35	-0.30	-0.37		-0.25	0.05	-0.64	79'0-	-0.02	-0.74	0.23		0.25	0.15	-0,11	1.09
Mass	Spec	4104 96	3103.20		1175.42	2084.42	2240.60	2691.91	1411,60		1447.65	1208.40	1222.35	1350.52	1384.59	1732.97	1060.20		1438.58	1566.76	1621.91	3407.77
Mass	Spec		CL.TUTT		1175.13	2084.16	2240,25	2691.61	1411.23		1447.40	1208.46	1221.71	1349.85	1384.57	1732.23	1060.43		1438.83	1566.92	1651.80	3408.86
ACC. No.		00000	P08112	Piol.					C27967	(Swiss-Prof)	•	JC4828 (PIR)					4557375	(NCBI)				
Species			CE LINE						bovins			нитап					hornan					
Mass Spec Species	Profile	,	5 peaks	match with TGF-82					2 peaks	match with SPP24		5 peaks snafch with histone H1.x					5 peaks	match with BIAP-3				
Band			72									25										

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Figure 164 Identification of Proteins by Mass Spectrometry of Tryptic Bragments from 1D Gels

				
Comments	% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)			
% Cover- age	27			
AAs	361-368	346-357	345-357	290-316
Mass Diff- erence	-0.09	0.12	0.11	127
Mass Spec		1438,5B	1568.75	3407.77
Mass Spec	1113.22	1438.70	1566.88	3408.04
Acc. No.	4557371 1113.22 (NCB)			
Species	human			
Band Mass Spec Species Acc. No.	4 peaks match with BMP-3	!		
Band	23			

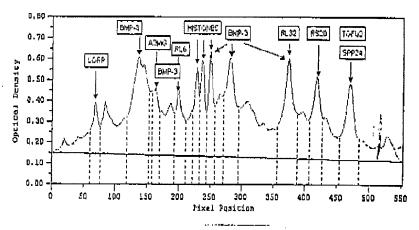


FIGURE 17A



FIGURE 178

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Figure 18 Quantitation of Identified BP proteins

Identified Protein	Percentage of Total Protein
LORP	2
вмР-3	11
BMP - 3 & A2-MG	3
RL6 & BMP-3	4
Histone	3 .
Histone	3
Histone & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
R\$20	5
SPP24 & TGF-β2	6
Total	58%

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Figure 19th Identification of Proteinsby Mass Spectrometry of Fragments from 2D Gels

										_						
Comments			•		peptide match continued by	इत्योग्द्राष्ट्र वाध्यक्ष										
*	Сочетаре		B				32		41							
AAs			472.487	368-382	N/A 488-504		241-253	648-659	105-116	58-70	21-33	301-314	318-334	274-285	239-261	0.41 131-154
		Diff	-0.13	0.51	NA		-0.31	0.26	0,46	0.14	0,36	1.06	0.71	1.40	09'G	
		Darlabase	1837.14	1921.14	NA		1509,86	2410.63	1406.80	1546,70	1660.60	1680.90	1834.00	2351.50	2380.70	2721.10
MS	Peaks	Dada	1837.01	1921,65	2679.51		1609,57	2410.89	1467.26	1546.BH	1661.16	16B1.85	1834.71	2352.90	2381.50	2721.51
Acc. No.			P05160 (Swiss- Prot)				NP002309 (Swiss- 1609,57 Prot)	•	P25975 (Swiss- Pmt)		•					
Species			Human				Нитап		Bovine							
Mass Spec			2 peaks malch with Coagulation	י מילים עוווח			2 peaks match with LORP		8 peaks match with Cathepsin 1 Precursor							•
5pol Digest	1		Lysc				Trypsin		Lysc							
1001			-				2		60							

Figure // Identification of Proteinsby Mass Spectrometry of Fragments from 2D Gets

Comments																					
*	Сочегаде		42				10			37											
AAS			26-31	32-37	BB-107	1-25	42-60			0.25 348-355	B1-01	286-296	0.02 249-260	103-114	103-115	34-49	.6 }- 0£	161-111	200-223	70-98	199-223
		Diff	-0.34	-0.25	-0.31	1.44	0.25	· — · · · · · · · · · · · · · · · · · ·		0.25	0.08	0.22	0.02	0.17	0.04	-0.16	-0.12	0.34	0.27	-0.49	-0.25
		Database	774.90	809.84	1175,43	3166,63	2187.51			917.14	984.15	1192.40	1380.65	1464.63	\$620.82	1779.00	2238.55	59.5262	2567.04	2898.43	2948.35
SMS	Peaks	Data	774.56	69.608	1175.12	3168.10	2187.77			917,39	984.23	1192.62	1380.87	1464.80	1620.86	1778.84	2238,43	2325.99	2661.31	2697.94	2946,10
Ace. No.			P21214 (Swiss- Pral)				O27967 (Swiss-	P.iot]	,	P39872 (Swiss- Prof)											
Species			Bovine				Bowine			Bovine											
Mass Spec	Profile		4 peaks malch with TGF-b2				1 peak	matches with SPP24		Trypsin 12 peaks match with ribosome									٠		
Digest			Lys.C							Trypsin			,	-							
Spot			2							6											

Figure #D Identification of Proteinsby Mass Spectrometry of Brzgments from 2D Gels

		Т		 -1	~														\neg)
Comments																					
*	Coverage		28	-						23				23							
AAs			19-26	152-161	151-161	174-185	94-108	199-212	65-81	34-46	62-79	64-79	1-21	230-239	134-144	230-241	198-210	37-48	221-239	66-22	
		Diff	-0.05	-0.02	0.13	0.00	J. 0.	-0.0g	-0.04	0,19	-0.01	-0.24	-0.38	0.10	00'0	0.42	0.12	-0.23	-0.24	-0.10	
		Dafabase	920.10	1218.31	1346.49	1516,69	1593.82	1720.00	1953,16	1327.58	1579,71	1707,89	2147.53	1168.38	1216.39	1353.61	1507.8B	1557.98	2140,58	2591.90	
MS	Peaks	Data	920.05	1218.29	1346.62	1516.69	1593.72	1719.91	1953,12	1327.75	1579.70	1707.65	2147.17	1168.48	1216.38	1354.03	1507.81	1557.75	2140.34	2591,60	
Acc. No.			P97351 (Swiss- Prol)							87558 (NCBI)				P12750 (Swiss- Prot)							
Species			Mouse							Нитва				Human							
Mass Spec	Profile		Trypsin 7 peaks match with ribosome	}						Trypsia 4 peaks match with histone H1.c				Trypsin 6 peaks match: Human with nbosume S4							
Digest .			Trypsin							Trypsin				Trypsin							
Spot			G)							ç				=							

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Figure 20 Quail Chorioallantoic Membrane (CAM) Angiogenesis Assay

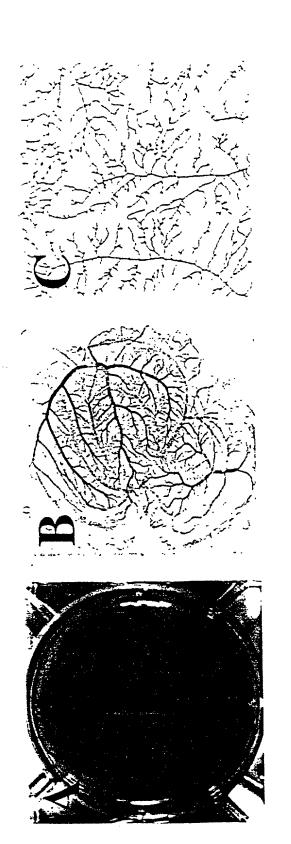


Figure 21 Black and white images of CAM vasculature after growth factor treatment

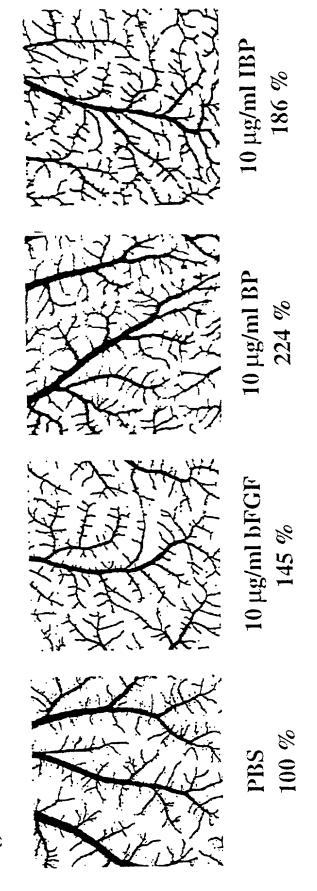
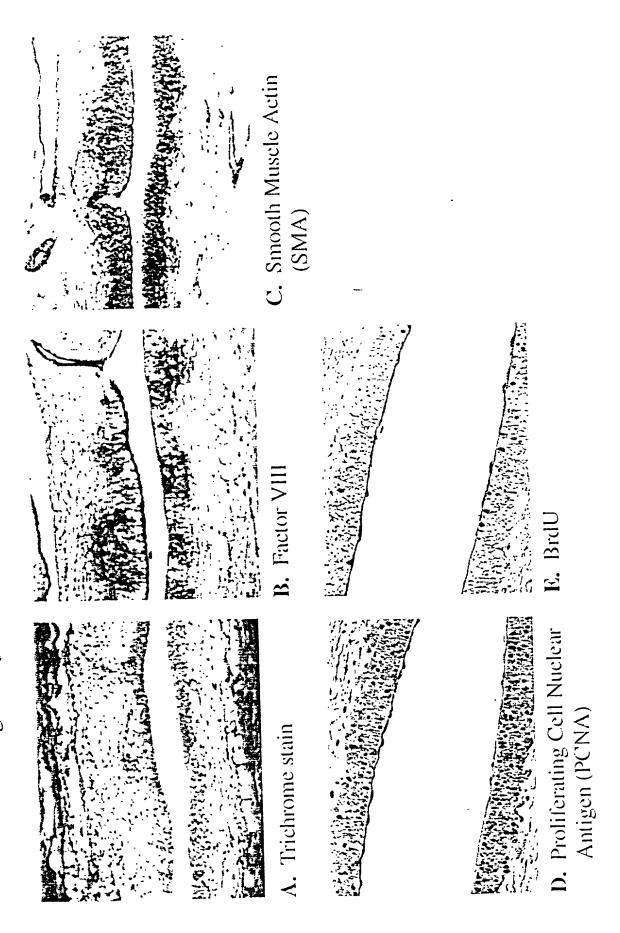


Figure 2.2 Histological sections of blood vessels formed in canine myocardium 2 weeks following BP injection



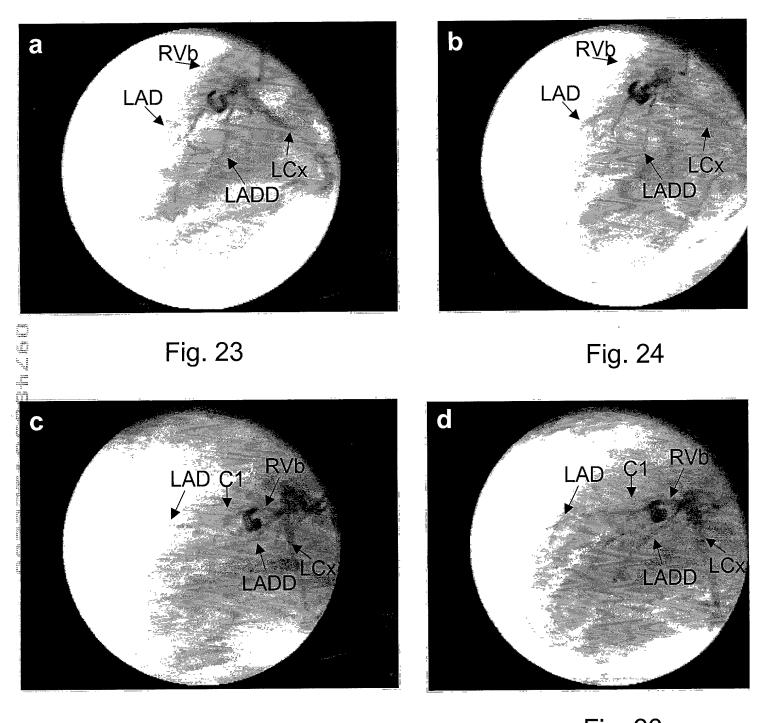


Fig. 26